



TOP PAGE | QUERY | RESULTS | PROJECTS | VIEWS | DATABANKS

HELP

Reset

View * Complete entries *

This entry is from: DDBJRELEASE:AE015074DDBJRELEASE

Save

Link

Launch

NCIustaIW

Printer Friendly

LOCUS AE015074 10085 bp DNA linear BCT 18-OCT-2002

DEFINITION *Shigella flexneri* 2a str. 301 section 37 of 412 of the complete genome.

ACCESSION AE015074 AE005674

VERSION AE015074.1

KEYWORDS

SOURCE *Shigella flexneri* 2a str. 301

ORGANISM *Shigella flexneri* 2a str. 301
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; *Shigella*.

REFERENCE 1 (bases 1 to 10085)

AUTHORS Jin, Q., Yuan, Z. H., Xu, J. G., Wang, Y., Shen, Y., Lu, W. C., Wang, J. H., Liu, H., Yang, J., Yang, F., Qu, D., Zhang, X. B., Zhang, J. Y., Yang, G. W., Wu, H. T., Dong, J., Sun, L. L., Xue, Y., Zhao, A. L., Gao, Y. S., Zhu, J. P., Kan, B., Chen, S. X., Yao, Z. J., He, B. K., Chen, R. S., Ma, D. L., Qiang, B. Q., Wen, Y. M., Hou, Y. D. and Yu, J.

TITLE Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity through comparison with genomes of *Escherichia coli* K12 and O157

JOURNAL Nucleic Acids Res. 30 (20), 4432-4441 (2002)

PUBMED 12384590

REFERENCE 2 (bases 1 to 10085)

AUTHORS Jin, Q., Shen, Y., Wang, J. H., Liu, H., Yang, J., Yang, F., Zhang, X. B., Zhang, J. Y., Yang, G. W., Wu, H. T., Dong, J., Sun, L. L., Xue, Y., Zhao, A. L., Gao, Y. S., Zhu, J. P., Chen, S. X., Yao, Z. J., Wang, Y., Lu, W. C., Qiang, B. Q., Wen, Y. M. and Hou, Y. D.

TITLE Direct Submission

JOURNAL Submitted (08-MAY-2001) Microbial Genome Center of Chinese Ministry of Public Health, 100 YingXin Jie, XuanWu Qu, Beijing 100052, P.R. China

FEATURES

source Location/Qualifiers

1..10085

/organism="Shigella flexneri 2a str. 301"

/strain="301"

/serotype="2a"

/db_xref="taxon:198214"

gene 91..795

/gene="adk"

/note="SF0419"

CDS 91..795

/gene="adk"

/note="Residues 2 to 234 of 234 are 98 pct identical to residues 1 to 233 of a 233 aa protein from *Escherichia coli* gb: AAB40228.1"

/codon_start=1

/transl_table=11

/product="adenylate kinase"

/protein_id="AAN42074.1"

/db_xref="GI:24050653"

/translation="MVVSFIAFSKKSTHFKGIFAMRIILLGAPGACKGTQAQFIMEKYGIPQISTGDMLRAAVKSGSELGKQAKDIMDAGKLVTDLVIALVKERIAEQDCRNGFLDGFPRTPQADAMKEAGINVDYVLEFDVPDELIVDRIVGRRVHAPSGRVYHVKNPDKVEGKDDVTGEELTTRKDDQEETVRKRLVEYHQMTAPLIGYYSKEAEAGNTKYAKVDG TKQVAEVRADLEKILG"

gene 927..1889

/gene="hemH"

/note="SF0420"

CDS 927..1889

/gene="hemH"

/note="Residues 1 to 320 of 320 are 98 pct identical to residues 1 to 320 of a 320 aa protein from *Escherichia*

coli 0157:H7 EDL933 ref: NP_286216.1"
/codon_start=1
/transl_table=11
/product="ferrochelatase: final enzyme of heme biosynthesis"
/protein_id="AAN42075.1"
/db_xref="GI:24050654"
/translation="MRQTKTGILLANLGTDPAPTPEAVKRYLKQFLSDRRVVDTSRLLWWPLLRGVILPLRSPRVAKLYASVWMEDGSPLMVYSRQQQALAQRLPDPVALGMSYGPSLESSVDELLAEHVDHIVVLPLYPQFSCSTVGAVWDELARILARKRSIPGISFIRDYADNHDYINALANSVRASFAGHGEPLDLLSYHGIPQRYADEGDDYPQRCRTTRELASALGMVPEKVMVMTFQSRFGREPWLMPYDTELKMLGEKGVGHIQVMCPGFAADCLETLEEIAEQNREVFLGAGGKKYEYIPALNATPEHIEMMANLVAAYR"
gene complement(2027..2845)
/gene="aes"
/note="SF0421"
CDS complement(2027..2845)
/gene="aes"
/EC_number="3.1.1.-"
/note="Residues 1 to 272 of 272 are 98 pct identical to residues 1 to 272 of a 319 aa protein from Escherichia coli K12 ref: NP_415009.1"
/codon_start=1
/transl_table=11
/product="putative lipase"
/protein_id="AAN42076.1"
/db_xref="GI:24050655"
/translation="MKPENKLPVLDLISAEMKTVVNTLQPDLPSPATGTIAEQRYQYTLERRFWNAGAPEMATRAYMVPTKYQVETRLFCPPQDPSATLFLYHGGGFI LGNLDTHDRIMRLASYSQCTVIGINYTLSPEARFPQAIIEEIVAACCYFHQQAEYDQINMSRIGFAGDSAGAMLALASALWLRDKQIDCGKIAGVLLWYGLYGLRDSVTRRLGGVWDGLTQQDLQMYEEAYLSNDADRESPPYCLFNNDLTREVPPCFIAGAEFDPLDDSRLLY"
gene 2997..4301
/gene="gsk"
/note="SF0422"
CDS 2997..4301
/gene="gsk"
/note="Residues 1 to 434 of 434 are 99 pct identical to residues 1 to 434 of a 434 aa protein from Escherichia coli 0157:H7 EDL933 ref: NP_286218.1"
/codon_start=1
/transl_table=11
/product="inosine-guanosine kinase"
/protein_id="AAN42077.1"
/db_xref="GI:24050656"
/translation="MKFPGKRKSKHYFPVNARDPLLQQFQPENETSAAWVVGIDQTLVDIEAKVDDFEIERYGLSAGHSLVIEDDVAEVLYQELKQKNLI THQFAGGTIGNTMHNSVLADDRSVLLGVMCSNIEIGSYAYRYLCNTSSRTDLNLYLQGVDPGIPGRCTFLIGESGERTFAISPGHMNQLRAESIPEDVIAGASALVLTSLYVRCKPGPEPMPEATMKAIEYAKKYNVPVVLTLGTGFVIAENPQWWQQFLKDHVSILAMNEDEAEALTGESDPLLASDKALDWVELVLCTAGPIGLYMAGFTEDEAKRKTQHPLLPGAIAEFNQYEFSRAMRHKDCQNPLRVYSHIAPYMGPEKIMNTNGAGDGALAALLHDITANSYHRSNPNSSKHKFTWLTYS SLAQVCKYANRVSQVLNQHSRPLTRGLPEREDSQEESYWDR"
gene complement(4434..6110)
/gene="ybaL"
/note="SF0423"
CDS complement(4434..6110)
/gene="ybaL"
/note="Residues 1 to 558 of 558 are 99 pct identical to residues 1 to 558 of a 558 aa protein from Escherichia coli 0157:H7 EDL933 ref: NP_286219.1"
/codon_start=1
/transl_table=11
/product="putative transport protein"
/protein_id="AAN42078.1"
/db_xref="GI:24050657"
/translation="MHHATPLITTIVGGLVLAFILGMLANKLRISPLVGYLLAGVLGPFTPGFVADTKLAPELAELGVILLMFGVGLHFS LKDLMAVKSIAIPGAIAQIAVATLLGMALSAVLGWSLMTGIVFGLCLSTASTVLLRALEERQLIDSQRGQIAIGWLI VEDLV MVLTLVLLPAVAGMMEQGDVGFATLAVDMGITIGKVIAFIAIMMLVGRRLVPWIMARS AATGSRELF TSVLALALGIAFGAVELFDVSFALGAFFAGMVLNESEL SHRAAHD TLP

LRDAFAVLFFVSVGMLFDPLILIQQLAVLATLAILFGKSVAAFLVRLFGHSQR
TLTAAASLAQIGEFALAGLGMALNLLPQAGQNLVLAGAILSIMLNPVLFALLEKYLA
KTETLEEQTLEEAIEEEKQIPVDICNHALLVGYGRVGSLLGEKLLASDIPLVVIETSR
TRVDELRRERGVRAVLGNAANEEMQLAHLECAKWLILTPNGYEAGEIVASARAKNP
DIEIARAHYDDEVYITERGANQVVMGERIARTMLELLETPPAGEVVTG"

gene complement(6348..7568)
/gene="fsr"
/note="SF0424"

CDS complement(6348..7568)
/gene="fsr"
/note="Residues 1 to 406 of 406 are 99 pct identical to
residues 1 to 406 of a 406 aa protein from Escherichia
coli O157:H7 EDL933 ref: NP_286220.1"
/codon_start=1
/transl_table=11
/product="fosmidomycin resistance protein"
/protein_id="AAN42079.1"
/db_xref="GI:24050658"
/translation="MAMSEQTQPVAGAAASTTKARTSFGILGAISLSHLLNDMIQSLI
LAITYPLLQSEFSLTFMQIGMITLTFQLASSLLQPVVGYWTDKYPMPWSLPIGMCF
TSLGLVLLALAGSFGAVLLAAALVGTGSSVFHPSESRVARMASGGRHGLAQSIFQV
GNGFSSSLGPLLAAVIIPYKGNVAVFWLAALLAIVVLAQISRWYSAQRHMNKGKPKAT
IINPLPRNKVVLAVSILLILIFSKYFYMASISSYTYFLMQKFGLSIQNAQLHLFA
FLFAV AAGTVIGGPVGDKIGRKYVWGSILGVAPFTLILPYARLHWTGVLTVIIGF
ILASAFS AILVYAQELLPGRI GMVSGLFFGFAGMGGLGA AVLGLIADHTSIELVYK
ICAFPLLL GMLTIFLPDNRHKD"

gene 7786..9438
/gene="ushA"
/note="SF0425"

CDS 7786..9438
/gene="ushA"
/note="Residues 1 to 550 of 550 are 99 pct identical to
residues 1 to 550 of a 550 aa protein from Escherichia
coli K12 ref: NP_415013.1"
/codon_start=1
/transl_table=11
/product="UDP-sugar hydrolase (5'-nucleotidase)"
/protein_id="AAN42080.1"
/db_xref="GI:24050659"
/translation="MKLLQRGVALALLTTFTLASETALAYEQDKYKITVLHTNDH
HGFWRNEYGEGYGLAAQKTLVDGIRKEVAAEGSVLLSSGGDINTGVPSDLQDAEP
DFRGMNLVGYDAMAGNHEFDNPLTVLRQKEKWKAFPLLSANIYQKSTGERLFK
PWFALFKR QDLKIAVIGLTTDDTAKIGNLEYFTDIEFRKPADEAKLVIQELQQTE
KPDIIIAATHM GHYDNGEHGSNAPGDVEMARALPAGSLAMIVGGHSQDPVCM
AAENKKQVDYVPGTPCK PDQQNGIWIQAHEWGKYVGRADFEFRNGEMKMVNYQL
IPVNLKKVTVWEDGKSERVL YTPETAEENQQMISLLSPFQNKGAQLEVKIGK
TNGRLEGGDRDKVRFVQTNMGRLLAA QMDRTGADFVMSGGGIRDSIEAGDISY
KNVLKVQPFGNVVYADMTGKEVIDYLTAV AQMKPDSGAYPQFANVSFVAKD
GKLNLDLIKGEVPDPAKTYRMATLNFNATGGDGYPR LDNKP
GYVNTGFI DA EVLKAYIQKSSPLDVSVYEPKGEVSWQ"

gene complement(9475..9954)
/gene="ybaK"
/note="SF0426"

CDS complement(9475..9954)
/gene="ybaK"
/note="Residues 1 to 159 of 159 are 100 pct identical to
residues 1 to 159 of a 159 aa protein from Escherichia
coli K12 ref: NP_415014.1"
/codon_start=1
/transl_table=11
/product="orf, conserved hypothetical protein"
/protein_id="AAN42081.1"
/db_xref="GI:24050660"
/translation="MTPAVKLLLEKNKISFQIHTYEHDP
AETNFGDEVVKLLGLNPDQV YKTLLEVAVNGDMKHLAVAVTPVAGQLDKK
VAKALGAKKVEADPMVAQRSTGYLVGG ISPLGQKKRLPTIIDAPAQEFAT
IYVSGGKRGDLIELAAGDLAKILDAKFADIARRD"

BASE COUNT 2628 a 2586 c 2607 g 2264 t
ORIGIN
1 gcatttttct tttcatcatc tgtactttcc gcaaattatc tcgccattaa cgttttcagg
61 ctccaggtgcc tttcttgagg caatgcctg ttgggtgat cgtttatcgc tttttcaaaa
121 aaatcgacac attttaagg gattttcgca atgcgtatca ttctgcttgg cgctccgggc
181 gcggggaaag ggactcaggc tcagttcatc atggagaaa atggtattcc gcaaatctcc

```
241 actggcgata tgcgtcggtgc tgcgggtcaaa tctggctccg agctgggtaa acaagcaaaa
301 gacattatgg atgctggcaa actgggtcacc gacgaactgg tgaatcgctg ggttaaagag
361 cgcattgctc aggaagactg ccgtaatggg ttccgtgttg accgcttccc gcgtaccatt
421 ccgcaggcag acgcgatgaa agaagcgggc atcaatgttg attacgttct ggaattcgac
481 gtaccggacg aactgattgt tgaatcgatc gtagggccgc gcgttcacgc gccgtctggt
541 cgtgtttatc acgttaaaat caatccgccc aaagtagaag gcaaagacga cgttaccggt
601 gaagaactga ctaccgctaa agacgatcag gaagaaaccg tgcgtaaacc tctggttga
661 taccatcaga tgactgcacc cgtgatcggc tactactcca aagaagcggg agcgggtaac
721 accaaatagc cgaaggtiga cggtagcaag caggttgctg aagttcgccg tgaatcgtaa
781 aaaatcctcg gctaatcaag ccgcagcaga tctgctttcg ggcagggtctg cttatccacc
841 tcaggcaata cctctcacag caattagttc ttcttctca cttttccgtc acaattatca
901 acaagtigaa tcgataagag gcggtaatgc gtcagactaa aaccggtatc ctgctggcaa
961 accitgggtac gcccgatgcc cccacacctg aagcggtaaa acgctatcgc aaacaaatftt
1021 taagcgacag acgcgtggtt gatacctcac ggttgttatg gtggccgttg ctgcccggcg
1081 tgattttgcc gctgcgctcg ccgcgtgtgg cgaagctgta cgctctgttc tggatggaa
1141 accgctcgcc gctgatggtt tacagccgcc agcaacagca ggcgttggca caacgtttac
1201 cggatagccc agtggcgctg ggcagtgcgt accgctcgcc atcactggaa agctccgtcg
1261 atgaactcct ggcagagcat gtatgcata ttgtgtgtgt gccgtttat cgcgaattct
1321 cctgttctac ggtcgggtgc gtatgggatg aactggcagc cattctggcg cgcaaacgta
1381 gcaatccggg gatatcggtt attcgtgatt acgcccagaa ccacgattac attaatgcac
1441 tggcgaacag cgtacgcgct tcttttgcca aacatggcga accggaatcg ctgctgctct
1501 cttatcatgg cattcccccag cgttatgcag atgaaggcga tgattaccgc caacgttgc
1561 gcacaacgac tgcgaactg gcttccgcac tggggatggt accggaaaaa gtagatga
1621 cctttcagtc gcgtttggc cgggaacctt ggcgatgccc ttataccgac gaacacgtga
1681 aaatgctcgc agaaaaaggc gtatgcata tacagggtat gtgcccggcg ttgtctgcgg
1741 attgtctgga gacgttggaa gagattgccg agcaaaaccg tgaggtcttc ctggttgcgg
1801 gcgggaaaaa atatgaatat attccagcgc ttaatgccac gccggaacat atcgaaatga
1861 tggctaactt tgttgcgcg tatcgctaaa gctgagcggg aaagaactga gcgccgtcgc
1921 gaagagcctc gtcggcggtt ttcatcatcc gtgaataatg caaaaaggca tgcagcgtag
1981 ctgggtagag ttgaactca cagggtcgtg gatcgccgcg taacgtctag taaagcagac
2041 ggcgtgcatc cagcagcggg tgaactccg ccccgcaat aaaacaggcg ggaacttgcg
2101 gagtgagatc attattaaac agacagtaat accgtgactc gcggtccgcg tctgtgctta
2161 aatacgctc ttcatatc tgcgaatcct gttgcgttaa gccatcccag acaccgccc
2221 acagacgacg agtcacggaa tcccgtaatc cgtaaagccc ataccacagc aaaacacccg
2281 caattttacc gcaatcgatc tgtttatcac gcaaccacaa cgcactggcg agcggcagca
2341 tggcacctgc ggaatcacgc gcaaaagcaa tgcgggacat attgattga taatctccg
2401 cctgctgggt gaaataacaa caagcagcca caatttctc tatcgcttgt ggaacacgcg
2461 cttcagggtg aagggtgtaa ttaatacaca tcaccgtaca ttggctgtag cttgccagca
2521 ggcgcatgat gcgatcgtg gtatcgagat tgcggagaat aaaacggcct ccatgcaaat
2581 aaaaatagct cggcgggcta tctggctcg gacaaaagag acgtgtttcc accgtgccat
2641 attttgttgg aacctgttaa gctctgttgc ccatcttgcg agcggccgca ttccagaatc
2701 ggcgctcaag cgtgtaatc tctgttgcg cagcaatcgt tccggttgcg ggccaggacg
2761 gtaaatcccg ctgaagagta ttcaaacagg tcttcatctc agcagaataa aggtccagaa
2821 caggtagttt gttttccggc ttcatacaaa aactccttc aaattacgtc attgtaagga
2881 accactgcca tgaaaatgcg atcccgcctg ctgatattga aactggctgc gttctgcgcg
2941 ctcccgtcag attgtgttaa cattcgccgc tcagttaacc acccgtaaaa acaaccaatga
3001 aatttcccgg taacgtaaaa tcaaacattt acttcccgtt aaatgcacgc gatccgctgc
3061 ttacgcaatt ccagccagaa aacgaaacca gcgcccgtcg ggtcgtaggt attgaccaga
3121 cgttggtcga tatgaagcg aaagtggatg atgaattcat tgagcgttat ggattagcg
3181 ccgggcattc actggtgatt gaggatgacg tagccgaagt gctttatcag gagctaaaac
3241 agaaaaacct gattacccat cagtttgcg gtggcaccat tggtaacacc atgcacaact
3301 actcgggtgt cgcggacgac cgttcgggtc tgcgtggcgt catgtgcagc aatattgaaa
3361 ttggcagtta tgcctatcgt tactgtgtga acacttccag ccgtaccgat cttaactatc
3421 tacaaggcgt gcatgggtcg attggctgtt gctttacgct gattggcgag tccggggaac
3481 gtacctttgc tatcagttca ggccacatga accagctgcg ggctgaaagc attccggaag
3541 atgtgattgc cggagcctcg gcactggttc tcacctcata tctgtgtcgt tgaacgccc
3601 gtgaacccat gccggaagca accatgaag ccattagta cgcaagaaa tataacgtac
3661 cgggtggtct gacgttggc accaagttt tcatgtccga gaatccgag tgggtggcagc
3721 aatttctcaa agaccacgtt tctatccttg cgtatgaacga agatgaagcc gaagcgttga
3781 ccggagaaag cgtatcgttg ttggcatctg acaaggcgtt ggaactgggt gagctggtgc
3841 tgtgcaccgc cgggcaatc ggcttgtata tggcgggctt taccgaagac gaagcgaaac
3901 gtaaaaccca gcatccgctg ctgcccggcg ctatagcgga attcaaccag tatgagttta
3961 gccgcgccat gcgccacaag gattgccaga atccgctgcg tcttatttcg cacattgcgc
4021 cgtacatggg cgggcgggaa aaaaatcatg acactaatgg agcgggggat ggccgatttg
4081 cagcgttgcg gcatgacatt accgccaaca gctaccatcg tagcaacgta ccaaaactca
4141 gcaaacataa attaccttgg ttaacttatt catcgttagc gcagggtgtg aatatgcta
4201 accgtgtgag ctatcaggta ctgaaccagc attcacctcg tttaacgccc ggcttgcgg
4261 agcgtgaaga cagccaggaa gactcttact gggatcggtt agttatcgtt ggttcgtagg
4321 ccagataagg cgttcacgcc gcatctggca ttgtgctctc gatgccgat gcgacgcttg
4381 cgcgtcttat catgcctaca tattttctat attttacatc cggcaaccac cgtttacccc
4441 gtcaccactt caccgcccgg tggcgtttcc agcagttcca gcatagtac ggcaatttca
```

4501 cgttcaccga tcaactacctg attcgcgcga cgttcgggtga tatacgtcac ttcacgtcga
4561 taatggggcgc gggcgataat ctcaatatcc ggggtttttcg cgcgggcaga cggcacaatc
4621 tcaccgcgtt cataaccgtt ggggatcgtc aggatcagcc attttgcaca ttcagatgt
4681 gccagttgca taatttcttc gttcgttga ttgcccata cagcgcggac cccacgtct
4741 cgcagctcat caaacgggt tctgtacgtc tcaatcaca ccagcggat atcagaggcg
4801 agcaatttct cccccagcag gctgcctaca cgaccgtaac ccaccaatag cgcattggtg
4861 caaatatcca ctgggatctg tttctcttct tcatgtgctt ctccacggt cgtctcttcc
4921 agcgtttcgg tcttcgccag atatttctcc agtagtgcca acagtaccgg gttgagcata
4981 atcgacagga tgccttcgtc cagtaccagg ttttgtccgg cctgcggcag taaatcaat
5041 gccattccca gtcccgccag gataaacgcg aactcaccaa tctgcgccag gctggcggcg
5101 atggttaatg ccgtacgttg ggagtgacca aacagacgga caaggaacag ggccgcgacc
5161 gatttaccaa acagaataat tgcagcgtc gccagcactg ccagcgggtg ctgaatcaga
5221 attaacggat caaacacat cccgactgag acaaaaaaca gcaccgcaa cgcgtcgcgc
5281 aatggcaacg tatcgtgggc ggcacgggtga ctcaattcag actcgttcag taccatcccg
5341 gcaaagaacg caccgagtc aaaggagaca tcaaacagct ctaccgcacc aaaggcaatc
5401 cctaacgcca gcgccagcac tgacagggtg aacagctcgc gagaaccggt tgcgcgctg
5461 cgtgccataa tccacggcac cagacggcga cctaccagca tcataatggc gataaatggc
5521 atcaccttgc cgtatgtgat ccccatatcg actgcaagag tggcaaaagg caccatcgcc
5581 tgttccatca ttcttgccac tgcgggcagc aacaccagcg tcagaacat caccaggtct
5641 tccacaatca accaaccgat ggcgatttgc ccacgtgac tgtctattaa ttgcccgtct
5701 tcaagtgcgc gcagtacac caccgtactg cgggtggaaa gacataagcc gaacacgata
5761 cgggtcatta acgaccagcc cagcagggcg gagagcgcca taccacgagc cgtcgccacg
5821 gctatctggg cgtatcgccc gggatggcg atggacttta ccgcatcaa atccttgagc
5881 gaaaaatgca aaccgacgcc gaacatcagc aaaataacgc ccagttcagc cagttccggc
5941 gcaagcttgg tatcgccaac aaagcccgga tgaatggtc ctgccagcac acccgtaac
6001 agatatccca ccagaggaga aatcagtagt ttattggcca gcatgccgag gataaaggcg
6061 agcacaaggc cgccaacaat ggtgggtgata agcgggggtg cgtgatgcat tccgtctctt
6121 tttcctgggt gttattgtcc attttgggtc gggaaaaaca aaattacagg tccattgcta
6181 tgacaatttc attgatgatg tttatgaata attgttgaat ttgcagaaa aatggaatta
6241 gctgcaaaaa aagcacggtt cggaaaacag aaggcggttt aacagaggaa aggcctatgg
6301 cgactgtaaa acgatgcagc caaagtttgc ctttggctgc aatgaaatca gtccttatgc
6361 cggttatcag gcaggaatat ggtcaacatc cccaatagtg gcaggaaaag acagatttta
6421 tagactaacg cgtatgctgt gtagtcggcg ataagcccca gaactgccgc tcccagacct
6481 cccatgccga aagcaaaacc gaaaaagagt ccagaaacca taccgatacg tccgggaagt
6541 agctccttag cgtagaccag aatggcagag aatgccgaag cgaggataaa tccaataatc
6601 accgttaaaa cccccgtcca gtgcaggcgg cgttagggta aaatcagcgt aaacggcgca
6661 acgcccagga tagagcccca aatcacatat ttccgtccaa ttttatccct tacaggcccg
6721 ccgatcacgc tacctgcgcg aacggcaaac aggaaggcaa acagatgaag ctgggcattc
6781 tggatagata atccgaattt ttgcatcaga taaaagggtg aatagctgct gatgctcgcc
6841 atatagaaat atttcgagaa aatgaggatt aacagaaatg tgactgccag taccactttg
6901 ttgcgcggca gtggattgat tatcgtcgtt ttgggttttc ctttatctat tgggtgctgt
6961 gccgagtacc aacggctaat ttgcgccaac accacgatcg ccacagtgcc cgcaagcaca
7021 aaccaggcaa cgttgccitt gccataaggc gcgataatca ccgccgccag caagggtccc
7081 agggaaactgc caaagttgcc gccgacctga aagatagatt gcgccaggcc atgccgccc
7141 ccggaagcca tacgggctac gcgagaagat tccgatgaa agaccgatga accggtaccg
7201 accagcgccg ctgccagcag aactgcgcca aaactgccc ccagcgcaag cagcaccaga
7261 ccacttaagg taaagcacat gccaatggc aacgaccacg gcatcgga taattatcggtc
7321 cagtagccga ccactgggtg cagtagcgaa gagggcagct ggaaggtag ggttatcatg
7381 ccaatctgca taaatgtcag agaaaattct gactgaagca gcggataaat cgcagaaatc
7441 agcgattgga tcatgtcgtt cagcagatgt gagaggctga tagcacctaa aataccaaac
7501 gatgttcggg ccttggctgt tgacgcagcc gcgcccgcga caggctgggt ttgttactc
7561 attgccatag gaaagtcact tttcagggt ttgcgatgaa agaattgatct tatttgtgat
7621 tattaccgga ctaacatacc tgtatgcgtc gctgaagga agtctcaac ccgaatacag
7681 aatttcta at ctggatcgag atttatcttc accggacgca gacttgtcta tgatgttgcg
7741 tcatactatt ttcaacacg ttgaaatcag gtcagggaga gaagtatgaa attattgcag
7801 cggggcgttg cgttagcgct gtttaaccaca tttaactgga cgagtgaac tgccttggcg
7861 tatgagcagg ataaaaacta caaaattaca gttctgata ccaatgatca tcatgggcat
7921 ttttggcgca atgaatatgg cgaatatggt ctggcgccgc aaaaaacgct ggtggatggt
7981 atccgcaaa aggttgcggc tgaaggcggt agcgtgtctg tactttccgg tggcgacatt
8041 aacactggcg tgcggagtc tgaattacag gatgccgaac ctgattttc cgttatgaa
8101 ctggttgggt atgacgcgat ggcgatcggt aatcatgaat ttgataatcc gtcaccgta
8161 ttacccagc aggaaaaagt ggcgaagttc ccgttgcttt ccgcaatat ctaccagaaa
8221 agtactggcg agcgcctgtt taaaccgtgg gcgctgttta agcgtcagga tctgaaaatt
8281 gccgttatgg gctgacaac cgatgacaca gcaaaaatig gtaacctgga atacttact
8341 gatatcgaat ttcgtaagcc cgccgatgaa gcgaagctgg tgattcagga gctgcaacag
8401 acagaaaagc cagacattat tatcgccggc acccatatgg ggcatlacga taatgtgag
8461 caccgctcta acgcaccgg cgatgtggag atggcacgcg cgtcgcctgc cggatcgctg
8521 gcgatgatcg tgggtgttca ctgcgaagat ccggtctgca tggcgccaga aaacaaaaaa
8581 caggctgatt acgtgccggg tacgccatgc aaaccagatc aacaaaacgg catctggatt
8641 gtgcaggcgc atgagtgggg caaatacgtg ggacgggctg attttgagtt tctaatggc
8701 gaaatgaaaa tggttaacta ccagctgatt ccggtgaacc tgaagaagaa agtgacctg

```
8761 gaagacggga aaagcgagcg cgtgctttac actcctgaaa tcgctgaaaa ccagcaaatg
8821 atctcgctgt tatcaccgtt ccagaacaaa ggcaaagcgc agctgggaagt gaaaaataggc
8881 aaaaccaatg gtcgtctgga aggcgatcgt gacaaagtgc gttttgtaca gaccaatatg
8941 gggcggttga ttctggcagc ccaaatggat cgcactggtg ccgactttgc ggtgatgagc
9001 ggaggcggaa ttctgtattc tatcgaagca ggcgatatca gctataaaaa cgtgctgaaa
9061 gtgcagccat tcggcaatgt ggtgggtgtat gccgacatga ccggtaaaga ggtgattgat
9121 taccigaccg ccgtcgcgca gatgaagcca gattcaggtg cctaccgcga atttgccaac
9181 gttagctttg tggcgaaaaga cggcaaacctg aacgacctta aaatcaaaagg cgaaccggtc
9241 gatccggcga aaacttaccg tatggcgaca itaaacttca atgccaccgg cggtgatgaa
9301 tatccgcgcc ttgataacaa accgggctat gtgaataacc gctttattga tgcggaagtg
9361 ctgaaagcgt atatccagaa aagctcgccg ctggatgtga gtgtttatga accgaaaggt
9421 gaggtgagct ggcagtaatc cgaaagtgcc gcatgtttgc atccggcaca atgcttaatc
9481 gcggcgggcg atatcagcaa atttggcadc gaggatcttt gccagatcgc ctgccgccag
9541 ttcgatatcc agtccgcgct tgcgcgccga aacataaata gtggcaaat ctgtgtcggg
9601 ggcgtcgata atcgttggca gacgtttttt ctgccccagt gggctaattc cccaaccag
9661 gtatcccgtc gaacgctgcg cgaccatcgg atcgccatc tcaactttct tggcaccag
9721 cgcttttgct acttttttaa gatccagttg acctgcgacc ggcgtaacgg ccacggcaag
9781 gtgtttcata tcaccgttca ctgccaccag cagcgttttg tagacctgat ccggattcaa
9841 acctaatttt ttgacgactt catcgccaaa attggtttca gccggatcgt gctcgtagg
9901 atggatttga aacgaaatct tgttttttc gagtaattta actgcgggtg tcatggtaat
9961 tticctgcct taaacaaaaa aacgaagcaa gcatacgctt gatggcggtc caaaaaaaag
10021 agtcacttgc cctaagagta ttggcaggat ggtgagattg agcgacaatc gagttacacc
10081 gtcgc
```

//

SRS 6.1.3.11 | [feedback](#)